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OM protein - protein search, using sw model

January 16, 2009, 16 39.12 , Search time 7.28471 Seconds (without alignments) 28.464 Million cell updates/see Pun on:

Title: $0S-09-856\cdot\hat{\sigma}7\hat{\sigma}-28$ Perfect score: 23Sequence: 1 MLRLQ 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	C83656 treponema p	ಾ				Q8uft9 agrobacteri		m	haemophilu	28yc62 brurella me	09pbb8 xyicila fas		'n	Q9alk4 raulobacter	~		_	PSÓ611 helicobarte	Q916b8 pastcurella	. —	F31976 bos taurus	F15311 homo sapien	P26040 mus musculu	209466 caenorhatett	09kv27 vibrio etal	Classe pseudomonas	Q09171 schizosacch	Q9v6a9 drosophila	083433 treponema p	Q9ks81 vitric chal	09pc09 xylella fas		m milderida castaso
		0.1	Y650 TRUDA	RI.19 HIIMAN	MLC1_HSVE4	UL51_HSVEB	PFF1_SCHPO	PYPH_AGRIF	PYRH_RH!ME	MTB1_NEIGO	MTH2_HAEAE	PYRH_BRIIME	PYRH_XYLFA	PYRB_RALSO	PYRH_RHILO	PYPR_CAMOR	PYRB_PSEAE	PYRR_PSEPU	YJIM KCOLI	FLGE_HFLMU	PUR1_PASMU	PUR1_HAEIN	EZRI_BCVIN	EZFI HIMAN	FZP1_MOUSE	Y⊋ ^e ∩_CAPTT	NUDC_VIBCH	LEP4_PSEST	ODPB_SCHPO	C49A_DROME	GAL1_TREPA	PURS_VIRCH	PUR2_XYLFA	YGW9_YEAST	GAPP PHIME
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0.417 Match. 130.6%, Scote 23: DB 1: Longth 160: Bost Local Similarity 100.0%; Pred. No. 13; Matches 5, Conservative 6, Mismatches 0, Indeis

QY 1 MLPLQ 5

RESULT 2

018192 caenorhabdi P77772 escherichia P32849 saccharomyc 090499 drosophila 090705 xenopus lac F41832 saccharomyc F3686 bacillus su F2671 vaccinia zi 69701 autopyrum p P33980 cautobacter P33980 cautobacter P3367 escherichia F16162 yersinia pe			oonema.	o., Sutton 6.6.,	Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardman J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Erchardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch H., Horst K., Roborts K., Sandusky M., Weidman J., Smith H.O.,	s, the syphilis	This JWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way medified and this statement is not removed usage by and for commercial entities requires a ilectuse direment (See http://www.isb-sib.ch/annonnector send an emmail to licensedisb-sib.ch).	: CRC64:
NH31_CABEL YPEF_ECOLI YPEF_ECOLI RADE_YEAST SWS_DROME NCQ_XENIA NCQ_XENIA NNI_YEAST PPRS_DACSU YPCL_XENIA PPRS_DACSU YPCL_XENIA PPRS_DACSU TOTHLYCOLY CHEN_CAUCH CHEN_CAUCH CHEN_CAUCH TOTHLYCOLI YED7_YERPE	ALIGNMEN'I S	ce u	TP0650. Troponema pallidum. Bacteria; Spirochaetales; Spirochaetaceae; Treponema NCBI_TaxID=160; [13]	9665876; Weinstock G.M., White	ey E.K., Clayton R., K 	"Competition of Stepanish pailidum, the Spirochete.", Science 281:375-388(1998).	copyright. It is producte of Bioinformatics os institute. There a littions as long as in it is not removed. Its contrament (See hith sealish-sib.ch).	1; 054. (054; 1. plete proteome. MW: 053796A8LA7L898F :R054:
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888 8388 8388 6444 600 644 644 644 644 644 644 644 64	RESULT 1 Y650_TREPA	083656; 30-MAY-2000 30-MAY-2000 16-001-2001 Hypothetical	TP0650. Treponema pa Bacteria; Sp NCB1_Tax1D=1	SEQUENCE FROM N.A. STRAIN-Nichols; Madiine-984442770; Frasci C.M., Norri	Dodson R., G Sodergren E. Khalak H., R McDonald L., Hatch B., Ho	Complete go spirochete." Srience 281:	This CWISS Perween the the European use by non modified and entities require the send an extendant entities to be send an extendant entities to be send an extendant entities to be send an extendant extendan	EMBL, AEDOSC TIGR; TPOOSC InterPro; IP Potate, PPOOS Proteon; PPOOS TIGREAMS; TI PROSTE, PSO Hypothetical SECUENCE
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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RX RUDIENE-21085665 PubMed 11217851;
RECIES-Monse: STRAIN-C57BL/6J:
RX RAWAI J., Shinadawa A., Shibata K., Yoshino M., Iroh M., Ishii Y.,
RA Ardawa I., Shinadawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
A Altawa E., Hara A., Ashburner M., Batalov S., Yasanaka I.,
RA Shito T., Okazaki Y., Gojobori T., Bono H., Kasuawa T., Saito R.,
RA Shito T., Okazaki Y., Gojobori T., Bono H., Kasuawa T., Saito R.,
RA Shito T., Okazaki Y., Gojobori T., Bono H., Kasuawa T., Saito R.,
RA Shito T., Okazaki Y., Sujuki R., Tomita M., Wagner I.,
RA Shimil L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Furumo M., Anno H., Haldarelli R., Barsh G.,
RA Sakai K., Okido T., Furumo M., Anno H., Haldarelli R., Barsh G.,
RA Sakai K., Okido T., Fletcher C., Fujina M., Gariboldi M.,
RA Suzuki M.J., Bult C., Fletcher C., Fujina M., Gariboldi M.,
RA Ordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Ordone P., Ring B., Ringwaid M., Penfighta Y., Storch R.-F.,
RA Sasaki H., Sato K., Schoenbach C., Spibata Y., Storch R.,
RA Sasaki H., Sato K., Schoenbach C., Spibata Y., Storch R.,
RA Winshaw-Boois A., Yoshida K., Haseqawa Y., Fawaji H., Rohlsaki S.,
A. Havashizaki V.
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"Nuclostide sequence of mouse L19 ribosomal protein cDNA isolated in
serrocring with tre oneogene probes.";
NNA Cell Hiol. 9:697-703(1990).
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                                                                                                                                                                                                                                                                                                                                                                 Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DPRT databases
                 RL19_HOMAN STANDARD; PRI; 196 AA. P1411B; P2290B; 01 JAN 1990 (Rel. 13, Created) 15AN 1990 (Rel. 14, Last sequence update) 15-JUN 2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 20:2598 2598(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Human;
MEDLINE-92285147; PubMcd-1598220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumabe T., Schma Y., Yamamoto L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer Res. 53:1403-1408(1993),
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB1_PaxID-9506, 10090, 10116;
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                                                                                                                                                                                       60S ribosomal protein 119.
RPL19.
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                          Chan Y.-L., Lin A., McNally J., Peleq D., Meyuhas O., Wool I.G., "The primary structure of rat ribosomal protein L19. A determination from the sequence of nucleotides in a cDNA and from the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Type 1 subtype 2).

Type 1 subtype 2).

Type 1 subtype 2).

Altinese: ASDNA viruses, no RNA stage; Herpesviridae;

Altinapherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                  chromosomal mapping, and novel promoter region.";
Genomics 25:372-380(1995).
-!- SIMILARITY: BELONGS TO THE LIPE FAMILY OF PIEOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                             Davies B., Fried M.:
"The L19 ribosomal protein gone (RPL19): gene organization,
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. AAP5063938526216 CRC64;
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01-DEC-1992 (Rel. 24, Last Sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
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Pfam; PF01280; Ribosomal_L19e; 1.
PROSITE; PS00526; RIBOSOMAL_L19E; 1.
                                                                                                                                        Biol. Chem. 262:1111-1115(1987).
                                                                                                                                                                                                                        SPECIES-Rat; STRAIN-Fischer; MEDLINE=95309903; PubMed=7789970;
MEDLINE-87109220; PubMed-3542997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X63527; CAA45090.1; -.
EMBL, S56985, AAR25672.1; -.
EMBL, BC000530; AAR100530.1; -.
EMBL; BC013016; AAR13016.1; -.
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                                                                                                             amino acids in the protein.
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FIR, A48992.
Genew: HGNC:10312; RPL19.
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8 OR H2.
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The DNA sequence of equine herpesvirus-1.";
Virology 189-304-316(1992)
-1- SIMILARITY - RELONGS TO FAMILY THAT GROUPS TOCPTHER HSV-1 (H.51).
                                                                           "Antigenic and protein sequence homology between VP13/14, a herpes
                                                                                                                                J. Virol. 65-2320-2326(1001)
-!- SIMILAKITY: BELONGS FO FAMILY THAT GROUDS TOOFTURE HSV-1 ULSI,
                                                                                           simplex virus type 1 tequment protein, and qp10, a glycoprotein of
                                      Whittaker G.R., Riggio M.P., Halliburton L.W., Killington R.A.,
Allen G.P., Meredith D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c`
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23, DB L, Length 244, 100 0%; Pred No 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190.0%, Score 23, DB 1, Length 245, 100.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                           211 AA: 26238 MW: 3F25(BPFARO4BOFFF CREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA; 2636F MW; 205RC04A882492A5 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine herpesvirus type 1 (strain Ab4p) (BHV-1)
Viruses, dSDNA viruses, no BNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ं
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Pel. 24, Created)
01-DEC-1992 (Pel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S, Misaalches
                     MEDLINE-91202570; PubMed-1850013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92295566; Puhmad-1418606.
                                                                                                              equine herpesvirus 1 and 4 ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M86664; AAB02443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               3est Local Similarity 100 0%.
                                                                                                                                                                                                                                                                                                                                                      EMBL; X17684; CAA35668.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                       EHV-1 8, AND VZV 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EHV-1 8, AND VZV 7
                                                                                                                                                                                                                                                                                                                                                                           $36703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136795; WZBEA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_Tax1D-31520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 MLRLQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 MLRLQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MI.RI.0 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLRLQ 5
                                                                                                                                                                                                                                                                                                                                                                         536703;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL51_HSVEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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RA Monday Compared Topological Residence of the Character C. Manillar E. Balandream M.A. Lype M., Lype R., Stewart A., Squiros J., Peal N., Hayles T., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Comnor W., Davis P., Fettwell T., Fraser A., Gentles S., Goble A., Hamfin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsky T., Howeith S., Muckle E.J., Hurt S., Jayers K., Anmes F., Jones M., Leather S., McChanl S., McLean J., Ra Anmes F., Moule S., Mondall S., McLeit D., Wiblett D., Odell C., Fa Allows E., Moule S., Saunders D., Stanger K., Sharp S., Ratherford K., Rutter S., Saunders D., Saunders D., Saunders B., Schorns E., Robert C., Taylor K., Taylor K.G., Tivoy A., Walsh S.V., Warron T., Whitehead S., Rodel C., Fuchs M., Fritze C., Bolzer E., Moestl D., Hilbert B., Rodel C., Fuchs M., Fritze C., Bolzer E., Moestl D., Hilbert B., Cabel C., Fuchs M., Braits C., Howell C., Mort E., Burnelle H., Mottier S., Gobel C., Robert M., Meeller Anner S., Gobel C., Robert M., Reibardt R., Mottier S., Ander D., Hilbert B., Calibert M., Meeller M., Mottier S., Ander D., Mark M., Meeller C., Mort E., Bank C., Mort E., Burnelle H., Mottier S., Ander D., Mark M., Meeller M., Mottier S., Childeau M., Callade L., Mortie S., Annatious J., Forsburg S.L., Elmique M., Redwelt M., Gallardin C., Hower T., McCombie W.R., Paulsen H., Mark M., Mallade M., Mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PRUL entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \dot{}
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                                                                                  15.UN-2002 (Rel. 41, Created)
15.JUN-2002 (Rel. 41, Last sequence update)
15.JUN-2003 (Rel. 41, Last sequence update)
15.JUN-2003 (Rel. 41, Last annotation update)
Serine/threomine-protein Finase pefi (BC 2.7.1.37) (Cyclin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 415:871-883(2062).
-- CATAVITIC ACTIVITY: AIP + a protein - ADP + a phosphoprotein.
-- SUBUNIT: Interacts with the past cyclin.
-- SUBUNIT: Extended with the past cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A pcl-like cyclin activates the Res2p-Cdc10p cell cycle 'start' transcriptional factor complex in lission yeast."; Mol. Biol. Cell 111.2845-2862(2000).
                                                                                                                                                                                                                                                                                   Edkaryota: Fungi, Ascompodu; Schizosaccharomycetes;
Schizosaccharomycetaics, Schizosaccharomycetaceae;
                                ZBB AA.
                                                                                                                                                                                                                                                     Schiggsacchiromyces pembe (Fission yeast).
                                PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20437747; PubMed=10982385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL031535; CAAZU75U.1; -.
                                                                                                                                                                                                   kinase pefl) (PHO85 homolog).
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lanaka Kili Okayana Hili
                                                                                                                                                                                                                                                                                                                                              Schrizosaccharomyces.
                                                                                                                                                                                                                             PEFI OR SPONING4.11.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCB1_Tax1D-4896;
                             PEF1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN 972
PEF1_SCHPO
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IPP002290; Ser_thr_pkinase

InterPro:

InterPro; IPR000719; Euk_pkinase.

EMBL; AB045127; HAH16402.1; -.

HSSP; P24941; 1CKP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood D.W., Setudal J.C., Raul R., Monks D.E., Kitajima J.P., Oktra V K., Zhou Y., Chen L., Weed C.E., Almeida N.F. Jr., Wee E., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Daatherage G., Gillet W., Grant C., Rutyavin T., Levy R., El M. J., McClelland E., Palmieri A., Raymond C., Konse G., Sacephimmarhak C., Wu X., Remeron P., Gordon D., Shang S., Yoc H., Tao Y., Biddle P., Judy M., Krespan W., Perry M., Cordon-Kamm H., Lido L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21608551; PubMed-11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Cordon B.S., Cao Y., Askenazi M., Halling C., Mullin L., Wollam C., Alling C., Mullin L., Wollam C., Allinger M., Boughty D., Srott C., Lappas C., Markelz B., Flandan C., Crowell C., Gitson J., Lome C., Sear C., Strub G., Cielo C., Slater S.; Cielo C., Slater S.; Cielo C., Slater S.; Artokacterium tumeraciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Carbamoy! phosphate + L-aspartate - phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciëns (strain C58 / ATCC 33970)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; Length 288; 100.0%; Pred. No. 25;
                                                                                                                                                                                                 Pransferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; indebs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamojltransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7A3077D33F40A8FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-carbamoyl-L-aspartate,
PATHWAY: Pyrimidiue biosynthesis: second step.
SIMILAKITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                              PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                    PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE: PSG0011: PROTEIN_KINASE_DOM; 1
PROSITE; PSO0108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21608550; PubMed-11743193;
Pfam, PF00069, pkinase, 1,
Proform, PD000001, Euk_pkinase, 1,
SMAKI, SMO0220, S_TKe, 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN 2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 17 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcarbamylase) (ATCase).
PYRB OR ATHI308 OR AGR_C_2407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:2417 2423(2091).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seienee 294:2323-2328(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                               Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 MLRLQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLRLU 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRB_AGRIS
                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                            BIND
                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORITET
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRB, AGRT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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between the Swiss Institute of Bioinformatics and the EMHL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. H.S.A. 98(9977-9882(2001).
-i- CAIALYLIC ACTIVITY: Carbamoyl phosphate ' Leaspartate - phosphate
                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boisard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godie T. Goffeun A., Rahn D., Kiss E., Lelaure V., Masuy D., Fohl T., Forfeteile D., Puchler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the lequme symbiont Proc Natl. Acad Sci H S.A. 98:9077-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium meliloti (Siborhizobium meliloti).
Bacteria; Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; Longth 414; 100.0%; Pred, No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 414;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                     Transferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrimidine biosynthesis; Transferase; Complete profeomé.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last. sequence update)
15-JUN-2002 (Rel. 41, Last. annolation update)
Aspartate carbamoyitransferase (RC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                   34055 MW; CA8BCB1948923BD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6E37984CBB5A6A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 AA
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                         EMBL; AE008058; AAK87099.1; ALT_INIT.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11GRFAMS; T1GR00670; asp_carb_tr; 1,
PROSITE; PS00097; CARBAMOYL.HANSFERASE; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23;
Pred. No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002029; Asp/Orn_COtrant.
InterPro; IPR002082; Asp_carbmltranst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21396507; PubMed-11481430;
                                                                                                                                                                                                                                                                                                 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: ALS91786; CAC45883.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcarbamylase) (AlCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02729; OFCace_N; 1.
                                                                                                                                          EMBL: AE009092; AAL42314.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRB OR R01304 OR SMC01360
                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                Fyrimidine blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam, Pf00185; ofCace;
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                   313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_Tax1D-382;
                                                                                                                                                                                                                                                                                                                                                                              222 MURIO 226
                                                                                                                                                                                                                                                                                                                                         1 MI.RI.Q 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRH_RHIME
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRH RHIME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein D.C., Gunn J.S., Piekarowicz A., "Sequence similarities between the genes encoding the S.Ngol and Hacii restriction/modification systems.", Blod. Chem. 379:575-578(1988).
    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; beta subdivision; Neisseriaggae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROGGCY, CAUSES SPECIFIC METHYLATION ON C-2 ON MOTH SIPANUS, AND PROFFCTS THE DNA FROM CLEAVAGE BY THE NGORI ENDONUCLEASE.

-! - CATALTIC ACTIVITY: S addrosyl Limorhioning + DNA cytosing = S-adenosyl L-homocyste eine + DNA 5 methylcytosing.

-! - SIMILARITY: BELONGS TO THE C5-METHYLTPANSPEPASE FAMILY.
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O
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                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40) Last sequence update)
16-OCT-2001 (Rel. 40) Last annotation update)
Medilication methylase NgoH (EC 2.1.1.73) (Cytosino specific
methyltransterase NgoH) (M.NgoH) (M.NgoH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Pel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Modification methylase Bacil (DC 2.1.1.73) (Cytosine specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 0% - Score 23; DB 1; Length 317.
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00094; C5_MIASE_1: 1.
PROSITE: PS00094; C5_MIASE_2: FALSE_NEG.
Transterase; Nethylliansterase; Restriction system.
ACT SITE:

PROSITE: PS00095; C5_MIASE_2: FALSE_NEG.
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                                                                                                                                                                                                         317 AA.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to licenseausb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT,
                                                                                                                                                                                                         PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98290322, PubMed-9628358,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPPO01525; C5_DNA_meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00145; DNA methylase; 1.
PRINTS; PR00105, CSMPTTPPRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                               16-00T-2001 (Fe! 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AA; 35944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity for ...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMRI : 1142459; AAR03206 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD,
  5; Conservative
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REBASE; 3607; M.NgoBI.
                                                                                                                                                                                                                                                                                                                                                                                      Neissoria qonorrhogan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_Tax1D-485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 MLRLQ 260
                                                                                       222 MLRIQ 226
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                                             1 MLRLQ 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN WR302
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030868;
                                                                                                                                                                                                      MTB1_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                             Hacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPOORNOR
                                                                                                                                                                                                                            059603;
                                                                                                                                                                                                                                                                                                                                                            NGOBÍM.
                                                                                                                                                                               MTB1_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTH2_HAEAE
  Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the bumpean Holinformatics institute. There are no restrictions on its use by non-picfit institutions as ing as its non-use in no way modified and this statement is not removed. Usage by and for commercial
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SIKAINTEM ZOOZOLOG, PUDMED-1756688.
MEDLINE-20020109; PubMed-1756688.
DelVecchio V.G., Kapairal V., Redkar R.J., Patra G., Mujer C., Los T., DelVecchio V.G., Kapairal V., Redkar R.J., Patrai A., Mijer C., Los T., Itakova N., Anivrsvn I., Phottacharyja A., Lykidis A., Remih S., Itakova N., Anivrsvn I., Phottacharyja A., Eykidis A., Remih S., Johnson B., Ishinovski I., Patrai N., Visoura M., Bermal A., Marur M., Soltsman B., Ishinovski I., Patrai S., OʻCallaghan D., Lottesson J.J.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPRAINT-ATCC 1116;
MEDLINE 98290312; PubMed-9628358;
Stein D.C., Gund J.S., Piekarowicz A.;
Stein D.C., Gund J.S., Piekarowicz A.;
"Sequence similarities between the genes encoding the S.Ngol and Hacli restriction/modification systems.";
Hiol. Chem. 379:575-578(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -: FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE STRANDED SEQUENCE FORGETY, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS, AND PROTECTS THE DNA FROM CLEAVAGE BY THE HABII ENDONUCLEASE.

-: CALALYTIC ACTIVITY: S addressyl-L-methicaline + DNA cytosine - S-adenosyl-L-momentance - DNA 5-methylogine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                            Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae;
Haemophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 0%; Score 23; DB 1; Length 318; 150.0%; Ptcd. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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15-JUN-2002 (Mel. 41, Last sequence update)
15-JUN-2002 (Pel. 41, Last unnotation update)
Asfaillate callamogilianistriase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Methyltransferase; Restriction system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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nethyltransferase Haell) (M.Haell).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interro, IPR001525; CS_DNA_meth.
Pfam; PP00145; DNA_methylase; 1.
PRINTS: PR00105; CSMETIRFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGKFAMS; TIGR00675; dcm; 1.
PROSITE: PS00094; C5_MTASE_1; 1.
PROSITE: PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AF019752; AA870829.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcarbamylase) (ATCase).
PYRB OR BMEI10670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO5102; 6MHT.
E; 3409; M.Haeil.
                                                             Haemophilus aegyptius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
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                                                                                                                                                              NCB1_Tax10-725;
                              HAELIM OR DOMA.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Simpson A.J.C., Reinach F.C., Arruda P., Abreu F.A., Acchecio M., Alvarenda R., Alves L.M.C., Arruda P., Abreu F.A., Acchecio M., Alvarenda R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonarcorsi E.D., Fordin S., Rovel J.M., Brioses M.E.S., Gherros M.H., Bonarcorsi E.D., Fordin S., Brother D.M., Carrer B., Colanto N.B., Colondo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coltino N.B., Colondo C., Costa F.F., Costa M.C.R., Forto C.M., Frada J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Frainca J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Frada J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Barincai M., Colondon G.H., Goldman M. B., Gomes S. L., Kitajima J.P., Krieger J.E., Kuramac E.E., Lambais M.R., Leite L.C.C., A Mireger J.E., Kuramac E.E., Lambais M.R., Leite L.C.C., A Machado M.A., Madeira A.M. B., Madeira A.M. B., Madeira A.M. B., Madeira A.M. B., Madeira B.C., Miyaki C.Y., Montelto L.E.S., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A. J., Nobrega F.G., Palmieri D.A., Paris A., Paris A.,
                                                    Proc. Natl. Acad. Sci. U.S.A. 99-442-448(2002)
-1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SdeS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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"The genome sequence of the facultative intraceilular pathogen
Brosella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Some 23; DR 1: Longth 322; 100.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00097; CARHAMOVIIRANSFERASE; 1.
Pyrimidine biosynthesis, Transferase, Complete protecume,
SEQUENCE 322 AA; 34802 MR; 8186208851895218 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slobul 10
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15 JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyllranslerase (EC 2.1.3.2) (Aspartate
                                                                                             -1- PATHWAY: Pyrimidine biosynthesis; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA
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                                                                                                                                                                                                                                                                                        InterPro: IPR002082; Asp_garbm!transf.
                                                                                                                                                                                                                                                                           InterPro: IPRO02024 - Asp./Orn_Cotranf
                                                                                                                                                                                                                                                                                                                                                HIGKFAMS; HIGRO0670; asp_carb_tr; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20365717; PubMcd-10910347;
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    N-carbamoyl-L-aspartate.

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                                                                                                                                                                                                                                                           EMBL; AE009702; AAL53912.1; -
                                                                                                                                                                                                                                                                                                                  Plam; PEO2729; OTGače_N, 1.
PRINTS: PRODION: AUTGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcarbamylase) (ATCase).
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nes 5: Conservative
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                                                                                                                                                                                                                                                                                                      Plam; PF00185; OTCace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 MIRIO 232
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                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
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Periode B.R., Fereira 3.A.G., Pereira H.A. Ji., Pesquero J.H., Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.G.F., da Silva T.R., Silva M.A. Jr., de Silva I.E., Silva I.E., Silva M.A. Jr., de Silvaira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., Varlada H., Van Sluys M.A., Verjovski-Ammeida S.M., Isuhako M.H., Van Sluys M.A., Verjovski-Ammeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C., The genome sequence of the plant pathogen Xylella Tastidiosa."; Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel Kenard C., Cunnac S., Demange N.,
Caspin C., Lavin M., Moisan A., Bobort C., Saurin W., Schicx T.,
Siquier P., Thebault M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.,
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Pyřímidine biosynthesis, second step.
-!- SUBUNIT: CONTAINS SIX CATALYTIC AND SIX REGULATORY CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S.,
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Bacteria: Protesbacteria, beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DH 1; Length 322; 100.0%; Pred. No. 28; ive 0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Translerase: Complete profeome
7 MW; DIDOESCC4F5A7MAD CRC64;
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Aspartate carbamor/transferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIGRPAMS; TIGPO0670; asp_carb_tr; 1. PSOGNOT: CARBAWYLTRANSFERASE; 1. Fyrimidic bicsynthesis; Translerase: Comp. SEQUENCE: 322 AA; 34637 MW; DIDDESCAPS,
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InterFro, IPR002081, Asp_carbmitrans1
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                                                                                                                                                                                                                                                                                                                                                                                                      N-carbamoyl-1.-aspartate.
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CAIALYIIC ACIIVIIY: Carbamoyl phosphate + L-aspartate - phosphate
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Phyllobacteriaceae: Mesorhizobium
NCBL_TaxID-381;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyltranslerase (EC 2.1.3.2) (Aspartate
                     PATHWAY: Pyrimidine biosynthesis: second step.
SIMILARITY: BELONGS TO THE APCASES/OPFASES FAMILY.
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PROSITE; PSO0097; CARBAMOYLTRANSFERASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR002029, Asp, orn_corranf.
InterPro, IPR002082; Asp_carbmltranst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002995; BAB48227.1; -.
InterPro: IPR002029; Asp./orn Cofranf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phizobium loti (Meserbirobium leti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-carbamoyl-L-aspartate.
· N-carbamoy1-1-aspartate.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AL646060; CAD14208.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ptam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcarbamylase) (ATCase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00100; ACTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plam; PF00185 offcace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5: Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 M:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRB OR MIR0686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 MI.RI.Q 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLPLQ 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYPR_PHILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRB_RHILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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This SWISS FPT early is empyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Except National Teach are as a textitutions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106.0%; Score 23; DB 1, Length 332; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lub.u%; Score 23; DB 1; Length 326; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; indeis
                                                                                                                                                                                                                                                PROSITE: PSOU097; CARBAMOTITRANSFERASE; 1.
Fyrimidine biosynthesis; Transferase, Complete proteome.
SEGENNOL 326 AA: 3511, MW, E75AUTHECOFFIES CROC4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS: TIGRU0670; asp_carb_tr; 1.
PROSTE; PS06977; CARRAMOVI.RARSERBASE; 1.
Pyrimidine Dosynthesis; Transferase, Complete profeome.
SEQUENCE 332 AA; 35509 MW; 13261cc5c13ElaR4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 JUN-2002 (kei. 4), Last sequence update)
15 JUN-2002 (Re). 41, Last annotation update)
Aspartate carbamegitransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Pyrimidine biosynthesis: second step.-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
InterPro: IPR002082; Asp_carbmltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPP002082; Asp_carbmltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPROU2029; Asp/Orn_Cotranf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPT;
                                                                                                                                                                                                               11@FFAMS; IIGP##570; asp_carb_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5-JUN-2002 (Rel. 41, Created)
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HSSP; P00479; 3CSU.

    N-carbamoyl-L-aspartate.

                                           Pfan, PF00185, OTCace; L. Pfan, PF00185, OTCace; L. Pfam, PF02729, OTCace_N; L. PPINTS: PF00100, AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pram; PFU2/29; OICade_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AIGC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINIS; PRO0100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDAPD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam; PF00185; Offace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                              query Match
Eest Local Similarity
5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Rost !cmal Sim!!arity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB1_Tax1D=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRB OR CC2443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 MEREO 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MI,RI,O 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYPR CAIICP
                                                                                                                                                                                                                                                                                                                                                                        MEDCENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN ATC 15692 / PAG1)
MEDIAN-C2647347; Pinded-10984043;
MEDIAN-C2647347; Pinded-10984043;
STOVET C.K. Phan X.-O.L. Evain A.L. Mizoguchi S.D. Warrener P.,
Bickey M.J. Brinkman F.S.L. Hulnagle W.O. Kowalik D.J. Lagrou M.,
Garber R.L., Golity L., Tolentino E., Westborck Wadman S., Yuan Y.,
Brody L.L., Coulter S.N. Folger K.P. Ras A. Larbig R. Lim R.M.,
Smith K.A., Speucer D.H., Wong G.K.-S., Wu Z., Paulson I.T.,
Roizer J., Saier M.H., Hannork R.F.W., Lory S., Olson M.V.;
"Complete genome sequence of Escudomonas actuainosa PAG1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:959-964(2000).
  Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ( N carbamoyl-L aspartate, PATHWAY: Pyrimidine biosynthesis; second step, SUBUNIT: HELEKODODECAMER OF 6 ACTIVE PYRB SUBUNITS AND 6 NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN ALCC 18692 / PAGT;
Vicktey J.F., Schutt M.J., Benjamin R.C., Cunin R., Shanley M.S.
                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; Length 334; 100.0%; Pred. No. 29; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrimidine biosynthesis, Transferase, Complete proteome.
CONFLICE 206 206 R -> A (IN REF. 1).
SEQUENCE 334 AA; 36629 MW; 2DC90450FA2E42E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                16 oct-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyltransterase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              !- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC PYRC' SUBUNITS (BY SIMILARITY)
                                                                                                                                                                           334 AA
Mismatchos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00670; asp_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002082; Asp_carbmitransf.
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                                                                                                                                                                           PRT;
                                                                                                                                                                                                                01-NoV 1997 (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF02729; OTCACC_N; 1.
                                                                                                                                                                                                                                                                                             transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: 1.19649; AAA25976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0100; AUTCASE.
5; Conservative
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ptam; PF00185; OfCace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00479; 3CSU
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-287;
                                                                           241 MLKLQ 245
                                                                                                                                                                                                                                                                                                             PYRB OR PA0402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Donovan G.A.
                                    1 MI.RI.Q 5
                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas.
                                                                                                                                                                           PYRB_PSEAE
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                                                                                                                                                        PYRB_PSEAE
Matches
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Gaps

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Best Local Similarity 100.0 Matches 5, Conservative

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Search completed: January 16, 2003, 16:51:16
                              237 MLRLQ 241
1 MLRLQ 5
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Job time . 9.28571 sees